

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Estu. 66:1 April 24, 2002, 08:55:22; South time 240.08 seconds (without alignments)

| | |
|----------------|-----------------------------|
| Title: | US-09-525-998A-1 |
| Perfect score: | 1368 |
| Sequence: | 1 suggested rearrangement |
| | ccccccctctctctccagatga 1368 |

Scoring table: IDENTITY_NUC

| Searched | 4,000,000 residues | Total number of hits satisfying chosen parameters |
|----------|--------------------|---|
| 1861242 | 1861242 | 1861242 |

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45

```

| | |
|-----|--|
| | NALgenes-11101 * |
| 1: | /SID82/qcadata/geneseq/geneseq/NAL980.DAT.* |
| 2: | /SID82/qcadata/geneseq/geneseq/NAL981.DAT.* |
| 3: | /SID82/qcadata/geneseq/geneseq/NAL982.DAT.* |
| 4: | /SID82/qcadata/geneseq/geneseq/NAL983.DAT.* |
| 5: | /SID82/qcadata/geneseq/geneseq/NAL984.DAT.* |
| 6: | /SID82/qcadata/geneseq/geneseq/NAL985.DAT.* |
| 7: | /SID82/qcadata/geneseq/geneseq/NAL986.DAT.* |
| 8: | /SID82/qcadata/geneseq/geneseq/NAL987.DAT.* |
| 9: | /SID82/qcadata/geneseq/geneseq/NAL988.DAT.* |
| 10: | /SID82/qcadata/geneseq/geneseq/NAL989.DAT.* |
| 11: | /SID82/qcadata/geneseq/geneseq/NAL990.DAT.* |
| 12: | /SID82/qcadata/geneseq/geneseq/NAL991.DAT.* |
| 13: | /SID82/qcadata/geneseq/geneseq/NAL992.DAT.* |
| 14: | /SID82/qcadata/geneseq/geneseq/NAL993.DAT.* |
| 15: | /SID82/qcadata/geneseq/geneseq/NAL994.DAT.* |
| 16: | /SID82/qcadata/geneseq/geneseq/NAL995.DAT.* |
| 17: | /SID82/qcadata/geneseq/geneseq/NAL996.DAT.* |
| 18: | /SID82/qcadata/geneseq/geneseq/NAL997.DAT.* |
| 19: | /SID82/qcadata/geneseq/geneseq/NAL998.DAT.* |
| 20: | /SID82/qcadata/geneseq/geneseq/NAL999.DAT.* |
| 21: | /SID82/qcadata/geneseq/geneseq/NAC2000.DAT.* |
| 22: | /SID82/qcadata/geneseq/geneseq/NAC2001.DAT.* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | | | | |
|---------------|--------|-------|--------|---------------------|
| Result No. | Score | Query | | Description |
| | | Match | Length | |
| 1 | 1366.4 | 99.9 | 1368 | Lambda-derived INF |
| 2 | 1366.4 | 99.9 | 1368 | Human TNFR1 coding |
| 3 | 1366.4 | 99.9 | 2088 | 30kD TNF inhibitor |
| 4 | 1366.4 | 99.9 | 2088 | AAO10883 |
| 5 | 1366.4 | 99.9 | 2111 | Human 30 kDa TNF i |
| 6 | 1366.4 | 99.9 | 2111 | Human Tumour necro |
| 7 | 1366.4 | 99.9 | 2161 | Human Tumour necro |
| 8 | 1364.8 | 99.8 | 2111 | Encodes human 55kD |
| 9 | 1363.2 | 99.6 | 2062 | p55 TNF-R gene, H |
| 10 | 1363.2 | 99.6 | 2062 | TNF-alpha binding |
| 11 | 1363.2 | 99.6 | 2176 | Encodes TNF-alpha |
| 12 | 1363.2 | 99.6 | 2176 | Type I TNF receptor |

Db 1145 cccatagccccctcttcttctctatgaactggccaaattctgtgccacctgtaagagag 1204
QY 940 qtaacacacccctatcaaaagagctaaacccatcttcaaacacacccctcaccctccacccc 999
Db 1205 qttqccccacccc--cagagctgctgaacctctctctacggatgctcacaacctatgcc 1261
QY 1000 atccccacccccctctcaagagtgagaga cagagacacaaagccacagagacctadac 1056
Db 1262 atccccccccctgttcaggaatcaggaagacgtcgtccagggccccagacagaggttacc 1321
QY 1057 actaatcaaccccccaacqctgtacgcctgtatagadaaacctaccccccttgcgctggaag 1116
Db 1322 actcaaacctcgatgctgtatgctgtggtgagtgctgctccagacagctggagag 1381
QY 1117 qaattcctacagccctaaagctaaacacacacagagatccatccqctggaqctacaaac 1176
Db 1382 qaattcctacagccctccagggctgaacacacacagagatccagggctggaqctggaac 1441
QY 1177 qagcgtgctgagagagagcaatacagctatctggagacctggagggcgagacgcgc 1236
Db 1442 agttatctccagagatctcattacagctatgtagaagcctgagagagagagagag 1501
QY 1237 cagcagaaacccacqctggaqctgttcaaacacqctacccagacatgaacctgctgagc 1296
Db 1502 cyagagagagagagagctgagctagtgagcgcgtgcttggagacatgaacctgctgagc 1561
QY 1297 tgcctaaagaaacatcgaagagagcctttacgcacccccc 1335
Db 1562 tgcctaaagaaacatcgaagagagcctttacgcacccccc 1600

Search completed: April 24, 2002, 05:14:46
Job time: 6564 sec